AORTIC CARBOXYPEPTIDASE-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING SAME

RELATED APPLICATIONS

This application claims priority to USSN 60/159,613 filed October 14, 1999, USSN 60/175,534, filed January 12, 2000, USSN 60/224,086, filed August 9, 2000 and 09/641,741 filed August 18, 2000 each of which is incorporated by reference in its entirety.

FIELD OF THE INVENTION

The invention relates in general to polynucleotides and polypeptides encoded thereby. The invention relates more particularly to nucleotides encoding polypeptides related to human aortic carboxypeptidase.

BACKGROUND OF THE INVENTION

The carboxypeptidases are a family of hydrolase enzymes that remove the amino acid at the free carboxyl (C) end of a polypeptide chain. Members of the carboxypeptidase family have been implicated in multiple biological activities.

Carboxypeptidases can be divided into at least two subfamilies of metallocarboxypeptidases. One subfamily includes the pancreatic carboxypeptidase-like subfamily. Its members include, *e.g.*, carboxypeptidase A, carboxypetpidase A2, carboxypeptidase B, and carboxypeptidase B2.

A second subfamily includes regulatory B-type carboxypeptidases. Its members include, *e.g.*, carboxypeptidase H, carboxypeptidease M , carboxypeptidase N, carboxypeptidase Z, AEBP1, ACPLX, Ms CPX1, and MsCPX2. Members of this subfamily have been implicated in activities that include regulation of polypeptide hormone processing activity and processing of extracellular peptides with carboxyterminal arginine residues. In addition, carboxypeptidases present at the surface of vascular smooth muscle cells, such as aortic smooth muscle cells, have been reported to exert a complex influence on the level of biologically active vasoactive peptides, *e.g.* bradykinin, angiotensin II, which influence the tone and caliber of blood vessels. Carboxypeptidases have also been reported to be responsible for a catabolic inactivation of vasoactive peptides.

Further, Manser et al. (1990) characterized a human and a rat brain cDNA that encodes carboxypeptidase E (CPE; EC 3.4.17.10). Naggert et al. (1995) stated that mice homozygous for the 'fat' mutation develop obesity and hyperglycemia that can be suppressed by treatment with exogenous insulin. The 'fat' mutation maps to mouse chromosome 8, very close to the gene for carboxypeptidase E (Cpe), which encodes an enzyme (CPE) that processes prohormone intermediates such as proinsulin. Naggert et al. (1995) demonstrated a defect in proinsulin processing associated with the virtual absence of CPE activity in extracts of fat/fat pancreatic islets and pituitaries. A single ser202-to-pro mutation distinguished the mutant Cpe allele and abolished enzymatic activity in vitro. Thus, the 'fat' mutation represents the first demonstration of an obesity-diabetes syndrome elicited by a genetic defect in a prohormone processing pathway.

Cool et al. (1997) noted that secretory proteins in general are released from cells via a nonregulated constitutive pathway; however, in neuroendocrine cells of the nervous and endocrine systems, there is also a regulated secretory pathway (RSP) from which hormones, neuropeptides, and the granins are secreted in a calcium-dependent manner. The larger inactive proforms of these peptide hormones and neuropeptides are packaged into the granules of the RSP and are processed to active peptides intragranularly, although early processing steps may occur at the trans-Golgi network. The specific sorting of RSP proteins away from those destined for the plasma membrane or other compartments, e.g., lysosomes, is an active and selective process requiring a sorting signal. A proposed mechanism for sorting secretory proteins into granules for release via the regulated secretory pathway involved binding the proteins to a sorting receptor at the trans-Golgi network, followed by binding and granule formation. Cool et al. (1997) identified such a sorting receptor as membrane-associated CPE in pituitary Golgi-enriched and secretory granule membranes. CPE specifically bound regulated secretory pathway proteins, including prohormones, but not constitutively secreted proteins. Cool et al. (1997) showed that in the Cpe(fat) mutant mouse lacking CPE, the pituitary prohormone, proopiomelanocortin (POMC), was missorted to the constitutive pathway and secreted in an unregulated manner. Thus, obliteration of CPE, the sorting receptor, led to multiple endocrine disorders of these genetically defective mice, including hyperproinsulinemia and infertility. (OMIM: http://www.ncbi.nlm.nih.gov/entrez/dispomim.cgi?id=114855)

The recent finding that Cpe(fat)/Cpe(fat) mice, which lack carboxypeptidase E (CPE) activity because of a point mutation, are still capable of a reduced amount of neuroendocrine

peptide processing suggested that additional carboxypeptidases (CPs) participate in this processing reaction. Searches for novel members of the CPE gene family led to the discovery of CPD, CPZ, AEBP1, and CPX-2.

Lei et al. (1999) described mouse CPX-1, another novel member of this gene family. Like AEBP1 and CPX-2, CPX-1 contains an N-terminal region of 160 amino acids with sequence similarity to the discoidin domain of a variety of proteins. The 410-residue CP-like domain of CPX-1 has 54% to 62% amino acid sequence identity with AEBP1 and CPX-2 and 33% to 49% amino acid identity with other members of the CPE subfamily. However, several active-site residues that are important for catalytic activity of other CPs are not conserved in CPX-1. Furthermore, CPX-1 expressed in either the baculovirus system or the mouse AtT-20 cell line does not cleave standard CP substrates. Northern blot analysis showed the highest levels of CPX-1 mRNA in testis and spleen and lower levels in salivary gland, brain, heart, lung, and kidney. In situ hybridization of CPX-1 mRNA in embryonic and fetal mouse tissue showed expression throughout the head and thorax, with abundance in primordial cartilage and skeletal structures. In the head, high levels of CPX-1 mRNA were associated with the nasal mesenchyme, primordial cartilage structures in the ear, and the meninges. In the thorax, CPX-1 mRNA was expressed in multiple developing skeletal structures, including chondrocytes and perichondrial cells of the rib, vertebral, and long-bone primordia.

Taken together, these findings suggest that it is unlikely that CPX-1 functions in the processing of neuroendocrine peptides. Instead, CPX-1 may have a role in development, possibly mediating cell interactions via its discoidin domain. (Lei et al. DNA Cell Biol 1999 Feb;18(2):175-85).

SUMMARY OF THE INVENTION

The present invention is based upon the discovery of novel human nucleic acid sequences encoding a polypeptides having sequence similarity to previously described members of the carboxypeptidase. The novel nucleic acids and ploypeptides are referred to herein as ACPL1, ACPL2, and ACPL3 nucleic acids and polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "ACPLX" nucleic acid or polypeptide sequences. For example, ACPLX nucleic acids include those found in SEQ ID NOS: 1, 3, 4, 5 and 7 and the corresponding polypeptides encoded by SEQ ID NOS: 2, 6, and 8.

Accordingly, one aspect of the present invention includes an isolated aortic carboxypeptidase-like nucleic acid molecule that includes a nucleotide sequence encoding a polypeptide that includes the amino acid sequence of SEQ ID NO:2. In various embodiments, the nucleic acid molecule can include a nucleotide sequence that includes SEQ ID NO:1. Alternatively, the encoded aortic carboxypeptidase-like protein (ACPLX) may possess a variant amino acid sequence, thereby having an identity or similarity less than 100% to the disclosed amino acid sequences.

The invention further includes an isolated polypeptide that includes the amino acid sequence of SEQ ID NO:2. Also included is a variant of a mature form of the amino acid sequence, or a variant of the amino acid, given by SEQ ID NO:2. In various embodiments, no more than 15 %, 10%, 9 %, 8%, 5%, 3%, 2%, or 1% of the amino acid residues in the sequence are changed to a different amino acid.

The invention yet further includes an antibody that immunospecifically binds to ACPLX. In the preferred embodiment, the antibody is monoclonal and of human origin. Such antibodies are most useful in treating a pathological condition in a subject wherein the treatment includes administering the antibody to the subject.

Also included in the invention is a method of producing an ACPLX by culturing a host cell expressing the aortic carboxypeptidase-like nucleic acids, described herein, under conditions in which the nucleic acid molecule is expressed.

The invention yet further includes a method of detecting the presence of an aortic carboxypeptidase-like polypeptide in a sample from a mammal, *e.g.*, a human, by introducing a sample from the mammal with an antibody that immunospecifically binds to one of the polypeptides, and then detecting the formation of reaction complexes including the antibody and the polypeptide in the sample. Detecting the formation of complexes in the sample indicates the presence of the polypeptide in the sample.

Also included in the invention is a method of detecting the presence of an aortic carboxypeptidase-like nucleic acid molecule in a sample from a mammal, *e.g.* a human, by introducing the sample with a nucleic acid probe that selectively binds to the nucleic acid, and then determining whether the nucleic acid binds to a nucleic acid molecule in the sample. Binding of the nucleic acid probe indicates the nucleic acid molecule is present in the sample.

The invention yet still further includes a method of identifying a potential therapeutic agent for use in the treatment of a pathology associated with altered levels of an aortic carboxypeptidase-like nucleic acid sample from a mammal *e.g.*, a human. The method

includes introducing a cell expressing the polypeptide with a composition that is a candidate substance for a therapeutic agent. Where the property or function of the candidate substance is altered in the presence of the cell, the substance is identified as a potential therapeutic agent.

The invention also includes a method of treating or preventing a pathological condition in a mammal *e.g.*, a human, associated with the polypeptide described herein, by administering to the subject an ACPLX in an amount sufficient to alleviate the pathological condition. Alternatively, the mammal may be treated by administering an antibody, as described herein, in an amount sufficient to alleviate the pathological condition.

Pathological states for which methods of treatment of the invention are envisioned include a cancer *e.g.*, breast and ovarian, hypertensive disorder, vascular endothelial disorders *e.g.* atherosclerosis, processing and/or transport of the vasopressin-neurophysin pre-hormone product.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a representation of an ACPL1a nucleotide sequence (SEQ ID NO:1) that encodes the ACPL1 polypeptide of the invention.

FIG. 2 is a representation of the ACPL1 polypeptide sequence (SEQ ID NO:2) encoded by the nucleotide sequence shown in FIG.1.

FIG. 3 is a comparison of the amino acid sequences of a mouse AEBP1 polypeptide (SEQ ID NO:9) ("Q61281"), a mouse aortic carboxypeptidase-like 2 polypeptide (SEQ

IDNO:10) ("O88442"), a human AEBP1 polypeptide (SEQ ID NO:11) ("Q14113"), a mouse carboxypeptidase X2 polypeptide (SEQ ID NO:12) ("O54860"), and the ACPL1a polypeptide of the invention (SEQ ID NO:2) ("ALO35460_GENESCAN_predicted_pep").

FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) and the ACPL1a polypeptide (SEQ ID NO:2) ("ALO35460_GENESCAN_predicted_pep").

FIG. 5 is a representation of a western blot showing expression of the ACPL1 polypeptide by 293 cells.

FIGS. 6A-6C are histograms representing relative expression of an ACPLX nucleic acid in various cell types and tissues.

FIGS. 7A-7C are histograms representing relative expression of an ACPLX nucleic acid of the invention in various tissues using a probe set AG86b.

FIG. 8 is a representation of an ACPL1b nucleic acid sequence (SEQ ID NO:3) which encodes the ACPL1 polypeptide of the invention given by SEQ ID NO:2.

FIG. 9 is a representation of an APCL2 nucleic acid sequence (SEQ ID NO:5) which encodes the ACPL2 polypeptide of the invention given by SEQ ID NO:6.

FIG.10 is a representation of the ACPL2 polypeptide sequence (SEQ ID NO:6) encoded by the nucleotide sequence shown in FIG.9.

FIG.11 is a representation of an ACPL3 nucleic acid sequence (SEQ ID NO:7) that encodes the ACPL3 polypeptide given by SEQ ID NO:8.

FIG.12 is a representation of the ACPL3 polypeptide sequence (SEQ ID NO:8) encoded by the nucleotide sequence shown in FIG.11.

FIG.13 is a representation of an ACPL1b nucleic acid sequence (SEQ ID NO:4) which encodes the ACPL1 polypeptide of the invention given by SEQ ID NO:2.

FIG. 14 is an illustration showing the results of a BLASTP search based on the ACPL2 polypeptide sequence (SEQ ID NO:6).

FIG. 15 is an illustration showing the results of a BLASTP search based on the ACPL3 polypeptide sequence (SEQ ID NO:8).

FIG. 16 is an illustration showing the results of a BLASTP search based on the ACPL1 polypeptide sequence (SEQ ID NO:2).

FIGS. 17A and 17B is a photograph of the Coomassie stained transfer on to a PVDF membrane of a tryptic digest of the polypeptide produced by clone pCEP4/Sec-AL035460, and the matching of the N-terminal sequence provided by Edman degradation of a tryptic peptide of approximately 40kDa (bottom row, gray) to the corresponding sequence of SEQ ID NO:2 (top row, black).

FIG. 18 is an illustration showing a ClustalW alignment of the ACPL1b protein sequence (SEQ ID NO:2), ACPL2 protein sequence (SEQ ID NO:6), and ACPL3 protein sequence (SEQ ID NO:8) of the present invention.

FIG. 19 is a bar chart showing the incorporation of BrdU into DNA induced by the carboxypeptidase produced by clone pCEP4/Sec-AL035460.

FIG. 20 is a bar chart showing NIH 3T3 cells induced by the carboxypeptidase produced by clone pCEP4/Sec-AL035460.

DETAILED DESCRIPTION OF THE INVENTION

The invention is based in part on the discovery of a novel nucleic acid sequences encoding novel polypeptides having amino acid sequences with significant similarities to the G aortic carboxypeptidase superfamily of proteins. The sequences are collectively referred to as "ACPLX nucleic acids" or "ACPLX polynucleotides" and the corresponding encoded

polypeptides are referred to as "ACPLX polypeptides" or "ACPLX proteins." Unless indicated otherwise, "ACPLX" is meant to refer to any of the novel sequences disclosed herein. The individual ACPLX nucleic acids and proteins are described below. Within the scope of this invention is a method of using these nucleic acids and peptides in the treatment, prevention or determination of a disorder associated with the polypeptides of the invention.

ACPL1

ACPL1 includes a family of three similar nucleic acids (refered herein as ACPL1a, ACPL1b and ACPL1c nucleic acids) encoding the identical ACPL1 polypeptide (SEQ ID NO:2) disclosed below.

ACPL1a

An ACPL1a nucleotide (alternatively referred to herein as AL035460A)is a 2382 bp long nucleic acid as shown in FIG. 1 (SEQ ID NO:1). The ACPL1a sequence present in AL035460A was derived from a genomic sequence obtained from chromosome 20 (20p12.3-13: GeneBank Accno. AL035460). The disclosed ACPL1a open reading frame ("ORF"), from 101 to 2305, begins at an ATG initiation codon at nucleotides 101-103 and terminates at a TGA codon at nucleotides 2305-07. A putative untranslated region upstream from the initiation codon is underlined in FIG. 1. The start and stop codons are in bold letters. The ORF encodes a polypeptide of 734 amino acid residues (FIG. 2; SEQ ID NO:2).

In a search of sequence databases, it was found, for example, that the disclosed ACPL1a nucleic acid sequence is identical at 1760 of 2129 bases (82% identity) to a 2379 bp *Mus musculus* metallocarboxypeptidase CPX-1 mRNA(GENBANK-ID: AF077738). The homology is present between bases 73 and 2201 of SEQ ID NO:1 and bases 112 and 2236 of the sequence of AF077738.

ACPL1b

An ACPL1b nucleotide (alternatively referred to herein as CG54007-01) is a 20,190 bp long nucleic acid (SEQ ID NO: 3) shown in FIG. 8. The disclosed ACPL1b open reading frame ("ORF") begins at an ATG initiation codon at nucleotides 1-3 and terminates at a codon at nucleotides 2202-04. The ORF encodes a polypeptide of 734 amino acid residues (FIG. 2; SEQ ID NO:2).

ACPL1c

An ACPL1c nucleotide (alternatively referred to herein as CG54007-06) is a 2205 bp long nucleic acid (SEQ ID NO:4) shown in FIG. 13. The ACPL1c nucleic acid sequence was

derived by laboratory cloning using exon linking. (See, Example 7). The disclosed ACPL1c open reading frame ("ORF") begins with a Kozak consensus ATG initiation codon at nucleotides 1-3 and ends with a TGA codon at nucleotides 2203-05. The start and stop codons are in bold letters. The ORF encodes a polypeptide of 734 amino acid residues (FIG. 2; SEQ ID NO:2).

In a search of sequence databases, it was found, for example, that the nucleic acid sequence of ACPL1c has 2204 of 2205 bases (99%) identical to a gb:GENBANK-ID:AX113925|acc:AX113925.1 mRNA from Homo sapiens (Sequence 1 from Patent WO0127290).

The full amino acid sequence of the ACPL1 protein was found to have 734 of 734 amino acid residues (100%) identical to, and 734 of 734 amino acid residues (100%) similar to, the 734 amino acid residue ptnr:SPTREMBL-ACC:Q9NUB5 protein from Homo sapiens (Human) (DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE carboxypeptidase CPX-1)); (FIG. 14) . The polypeptide of SEQ ID NO.:2 is predicted by the program PSORT to localize extracellularly with a certainty of 0.6520. The program SignalP predicts that a signal peptide exists, with the most likely cleavage site occurring between residues 20 and 21 of SEQ ID NO: 2, i.e., at the "-" in the sequence ALG-AP.

The encoded amino acid sequence (SEQ ID NO.: 2) is also related to murine metallocarboxypeptidase CPX-1 (SPTREMBL-ACC:Q9Z100), which is a polypeptide of 722 residues. 622 of 733 residues (84%) of the encoded ACPL1a polypeptide are identical to, and 661 of 733 residues (90%) positive with, the murine metallocarboxypeptidase CPX-1 polypeptide. The disclosed ACPL1 polypeptide sequence (SEQ ID NO:2) includes additional residues not found in ACC:Q9Z100. The disclosed ACPL1 polypeptide also includes sequences related to the 764 residue murine carboxypeptidase X2 (SPTREMBL-ACC:O54860). For the regions 41-733 of the disclosed ACPL1 polypeptide and residues 61-759 of murine carboxypeptidase X2, 377 of 698 residues (54%) are identical to, and 486 of 698 residues (69%) are positive.

A multiple sequence alignment between the disclosed ACPL1a polypeptide (SEQ ID NO.: 2) and other carboxypeptidase family members is presented in FIG. 3. Shown is a comparison of the amino acid sequences of a mouse AEBP1 polypeptide (SEQ ID NO.: 9), ("Q61281"); a mouse aortic carboxypeptidase-like 2 polypeptide (SEQ ID NO.: 10), ("O88442"); a human AEBP1 polypeptide (SEQ ID NO:11) ("Q14113"); a mouse

carboxypeptidase X2 polypeptide (SEQ ID NO: 12), ("O54860"); and the ACPL1 polypeptide of the invention (SEQ ID NO:2) ("ALO35460_GENESCAN_predicted_pep").

The disclosed ACPL1 polypeptide (SEQ ID NO.: 2) is identical at 202 of 366 residues (55%) to, and positive at 260 of 366 residues (71%) with, the Q61281 protein (SEQ ID NO.: 9). The protein encoded by SEQ ID NO.: 9 is described in Nature 378:92-96, 1995.

The disclosed ACPL1 polypeptide (SEQ ID NO.: 2) is identical at 334 of 623 residues (53%) to, and is positive at 433 of 623 residues (69%) with, the O88442 protein (SEQ ID NO.: 10). The protein encoded by SEQ ID NO.: 10 is described in J. Biol. Chem. 273:15654-60, 1998.

The disclosed ACPL1 polypeptide (SEQ ID NO.: 2) is identical at 224 of 408 residues (54%) to, and positive at 286 of 408 residues (70%) with, the Q14113 protein (SEQ ID NO.: 11). The protein encoded by SEQ ID NO.: 11 is discussed in Biochem Biophys. 228:411-14, 1996.

The disclosed ACPL1 polypeptide (SEQ ID NO.: 2) is identical at 377 of 698 residues to (54%) and is positive at 486 of 698 residues (69%) with, the O54860 protein (SEQ ID NO.: 12).

FIG. 4 shows that the disclosed ACPL1 polypeptide (SEQ ID NO.: 2) is also highly similar to murine CPX-1. Shown is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) (SEQ ID NO.: 13) and the ACPL1a polypeptide (SEQ ID NO:2) ("ALO35460_GENESCAN_predicted_pep").

The disclosed ACPL1 polypeptide sequence (SEQ ID NO.: 2) includes multiple domains. These domains are shown in FIG. 2. These include an amino-terminal signal peptide-like sequence, a 161-residue discoidin domain and two carboxypeptidase (CP) catalytic cleavage domains with zinc binding residues. The first CP domain is at residues 299-409, and the second CP domain extends over residues 421-689. Also present in the disclosed ACPL1 polypeptide is a calcium-binding site that is highly conserved among the metallocarboxypeptidase family members.

The sequence homologies demonstrate that ACPLX is a member of the regulatory B-type carboxypeptidase subfamily and can be considered, *e.g.*, a human ortholog to murine CPX-1. The relationship between the new polypeptides and other regulatory B-type carboxypeptidases is presented in Table I.

Table I. The two metallocarboxypeptidase subfamilies.

Pancreatic carboxypeptidase-like subfamily.

Carboxypeptidase A	Pancreatic-digestive
Carboxypeptidase A2	Pancreatic procarboxypeptidase acts on aromatic C-terminal residues.
Carboxypeptidase B	Pancreatic-digestive
Carboxypeptidase B2	(U) Thrombin-activatable fibrinolysis inhibitor (TAFI) (plasminogen activator)

The regulatory B-type carboxypeptidase subfamily.

Carboxypeptidase E	(CBPE) Processes prohormone intermediates such as proinsulin (Fricker, et al., Trends Biochem Sci.24 :390-93, 1999).
Carboxypeptidase M	Regulates peptide hormone activity (Rehli et al., J Biol Chem. 270:15644-49, 1995).
Carboxypeptidase D	A homolog of duck gp180, a 180 kDa hepatitis B virus-binding protein (McGwire et al., Life Sci. 60:715-24, 1997).
Carboxypeptidase N	Cleaves and inactivates kininase-1 and anaphylatoxin in the serum (Tan et. al., Anesthesiology 70:267-75, 1989).
Carboxypeptidase Z	May process extracellular peptides or proteins with C-terminal Arg residues (Song et al., J Biol Chem. 272:10543-50, 1997).
AEBP1	Regulates transcription by cleavage of factors involved in transcription (Muise, et al., Biochem J. 343:341-45, 1999).
ACPLX	Functioning of differentiated vascular smooth muscle cells (Layne, et al., J. Biol. Chem. 273:15654-60, 1998).
Ms_CPX2	Possibly acts as a binding protein rather than as an active carboxypeptidase (Xin, et. al., DNA Cell Biol 17:897-909, 1998).
Ms_CPX1	May have a role in development by mediating cell interactions via its discoidin domain (Lei , et al., DNA Cell Biol. 18:175-85, 1999).

The CP domains have 95 and 91% amino acid identity, respectively (see Table II), with CPX-1, a mouse homolog that lacks several active-site residues that are important for catalytic activity (Lei , et al., DNA Cell Biol. 18:175-85, 1999). The catalytic sites that are absent in CPX-1 are also absent in the carboxypeptidase-like proteins of the present invention, indicating that an ACPLX polypeptide according to the invention may lack enzymatic

cleavage function. However, a zinc-binding region, absent in most human metallocarboxypeptidases, is present in both the protein of the present invention and CPX-1. The zinc-binding region is located within the second catalytic domain at H498 and H491, respectively, of the two polypeptides. The function of this extra zinc binding domain is unknown may serve as an additional enzymatic site on the molecule.

The extent of sequence homology between members of metallocarboxypeptidase family members and an ACPLX polypeptide of the invention is shown Table II.

Table II. Protein domain sequence homology between members of the metallocarboxypeptidase family and the polypeptides encoded by ACPLX.

Gene ID	Total	Discoidin	Ca	1st CP	2nd CP	Zn
Hu_CBPA	POOR----------					
Hu_CBPA2	POOR----------					
Hu_CBPB	POOR----------					
Hu_CBPB2 (U)	POOR ----------					
Hu_CBPH (E)	50%	5%	77%	**74%**	**67%**	Y
Hu_CBPM	POOR	0%	46%	66%	59%	Y
Hu_CBPD	POOR	12%	77%	54%	43%	Y
Hu_CBPN	POOR	16%	15%	74%	62%	N
Hu_CBPZ	POOR	13%	69%	54%	48%	Y
Hu_AEBP1	53%	52%	92%	71%	54%	N
Hu_ACPLX(sgnl)	53%	51%	92%	71%	54%	N
Ms_AEBP1	54%	40%	85%	70%	54%	N
Ms_ACPLX	54%	53%	85%	70%	48%	N
Ms_CPX2	58%	58%	85%	71%	57%	N
Ms_CPX1	**86%**	**87%**	**92%**	**95%**	**91%**	**Y**
Ms_CBPH (E)	POOR	5%	77%	74%	65%	Y

Hu = human
Ms = mouse
POOR = ≤50% match over full length
Total = % identity over the full-length protein sequences.
The remaining values are sorted as % homology within specific domains.
Ca = Calcium binding region.
1st CP = First carboxypeptidase catalytic domain (residues 299-409).
2nd CP = Second carboxypeptidase catalytic domain (residues 421-689).
Zen = Presence (Y) or absence (N) of the 3rd catalytic zinc binding site.

Based on a comparison of the first and second CP domains between the protein of the present invention and members of the human carboxypeptidase family, the disclosed ACPL1 polypeptide (AL035460A protein) (SEQ ID NO.: 2) shares most sequence identity with carboxypeptidase E (hu_CBPH(E)). The percent identity for the first and second CP regions is 74 and 67%, respectively. CPE is a pro-hormone processing enzyme and is responsible for the production of insulin from its precursor pro-insulin. Mice expressing a mutant variant of CPE have improper insulin regulation with a resulting phenotype of obesity and hyperglycemia that can be suppressed by treatment with exogenous insulin (Naggert, et. al., Nature Genet. 10:135-142, 1995).

Although the disclosed ACPL1 polypeptide (SEQ ID NO.: 2) shows some similarity to hu_CPE at the catalytic site, the disclosed ACPL1 polypeptide (SEQ ID NO.: 2) differs greatly at the amino-terminus. For example, a discoidin domain is present in the disclosed ACPL1 polypeptide, but is absent in hu_CPE. Discoidin domains on proteins allow the protein to interact with collagen on the surface of cells which mediates cell surface interactions between receptors and ligands (Vogel, FASEB J.13:S77-82,1999).

ACPL2

The disclosed ACPL2 (alternatively referred to herein as CG54007-04) includes the 1725 nucleotide sequence (SEQ ID NO: 5) shown in FIG. 10. A ACPL2 ORF begins with a initiation codon at nucleotides 1-3 and ending at nucleotides 1723-25. The ACPL2 polypeptide (SEQ ID NO: 6) encoded by SEQ ID NO: 5 is 574 amino acids in length, and is presented using the one-letter amino acid code in FIG. 11. The polypeptide of SEQ ID NO.: 6 is predicted by the program PSORT to localize extracellularly with a certainty of 0.6520. Further, the program SignalP predicts that a signal peptide exists, with the most likely cleavage site occurring between residues 20 and 21 of SEQ ID NO: 6, *i.e.*, at the "-" in the sequence ALG-AP.

In a search of sequence databases, it was found, for example, that the nucleic acid sequence of ACPL2 has 1544 of 1555 bases (99%) identical to a gb:GENBANK-ID:AK027661|acc:AK027661.1 mRNA from Homo sapiens (Homo sapiens cDNA FLJ14755 fis, clone NT2RP3003145, moderately similar to Mus musculus metallocarboxypeptidase CPX-1 mRNA). The full amino acid sequence of the ACPL2 protein of the invention having 574 amino acid residues was found to have 510 of 510 residues (100%) identical to, and 510 of 510 amino acid residues (100%) similar to, the 734 amino acid residue ptnr:SPTREMBL-

ACC:Q9NUB5 protein from Homo sapiens (Human) (DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE carboxypeptidase CPX-1))) (Fig. 14).

A search of the databases such as Pfam, PROSITE, ProDom, Blocks or Prints revealed the presence of identifiable domains in the ACPL2 polypeptide sequence as summarized in Table III.

Table III.

ACPL2

Model	Description	Score	E-value	N
F5_F8_type_C (InterPro)	F5/8 type C domain	151.4	1.6e-41	1
Zn_carbOpept (InterPro)	Zinc carboxypeptidase	100.4	3.4e-26	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
F5_F8_type_C	1/1	117	271 ..	1	158 []	151.4	1.6e-41
Zn_carbOpept	1/2	299	416 ..	1	118 [.	75.1	2.5e-19
Zn_carbOpept	2/2	475	509 ..	50	86 ..	25.3	7.5e-06

The domains identified in Table III. are described as follows:

IPR000421 Coagulation factor 5/8 type C domain (FA58C): Blood coagulation factors V and VIII contain a C-terminal, twice repeated, domain of about 150 amino acids, which is called F5/8 type C, FA58C, or C1/C2- like domain. In the slime mold cell adhesion protein discoidin, a related domain, named discoidin I-like domain, DLD, or DS, has been found which shares a common C-terminal region of about 110 amino acids with the FA58C domain, but whose N-terminal 40 amino acids are much less conserved. Similar domains have been detected in other extracellular and membrane proteins. In coagulation factors V and VIII the repeated domains compose part of a larger functional domain which promotes binding to anionic phospholipids on the surface of platelets and endothelial cells. The C-terminal domain of the second FA58C repeat (C2) of coagulation factor VIII has been shown to be responsible for phosphatidylserine-binding and essential for activity. It forms an amphipathic alpha-helix,

which binds to the membrane. FA58C contains two conserved cysteines in most proteins, which link the extremities of the domain by a disulfide bond. A further disulfide bond is located near the C-terminal of the second FA58C domain in MFGM.

IPR000834 Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family: The carboxypeptidase A family (M14) can be divided into two subfamilies: carboxypeptidase H (regulatory) and carboxypeptidase A (digestive). Members of the H family have longer C-termini than those of family A, and carboxypeptidase M (a member of the H family) is bound to the membrane by a glycosylphosphatidylinositol anchor, unlike the majority of the M14 family, which are soluble. The zinc ligands have been determined as two histidines and a glutamate, and the catalytic residue has been identified as a C-terminal glutamate, but these do not form the characteristic metalloprotease HEXXH motif. Members of the carboxypeptidase A family are synthesised as inactive molecules with propeptides that must be cleaved to activate the enzyme. Structural studies of carboxypeptidases A and B reveal the polypeptide to exist as a globular domain, followed by an extended alpha-helix; this shields the catalytic site, without specifically binding to it, while the substrate-binding site is blocked by making specific contacts.

ACPL3

The disclosed novel ACPL3 (alternatively referred to herein as CG54007-05) includes the 1972 nucleotide sequence (SEQ ID NO: 7) shown in FIG. 12. An ACPL3 ORF begins with initiation codon at nucleotides 1-3 and ending at nucleotides 607-09. The ACPL3 polypeptide (SEQ ID NO: 8) encoded by SEQ ID NO: 7 is 202 amino acids in length, and is presented using the one-letter amino acid code in FIG. 13.

In a search of sequence databases, it was found that the nucleic acid sequence of ACPL3 has 1404 of 1407 bases (99%) identical to a gb:GENBANK-ID:AK027661|acc:AK027661.1 mRNA from Homo sapiens (Homo sapiens cDNA FLJ14755 fis, clone NT2RP3003145, moderately similar to Mus musculus metallocarboxypeptidase CPX-1 mRNA). The full amino acid sequence of the ACPL3 protein having 202 amino acid residues was found to have 192 of 193 amino acid residues (99%) identical to, and 193 of 193 amino acid residues (100%) similar to, the 734 amino acid residue ptnr:SPTREMBL-ACC:Q9NUB5 protein from Homo sapiens (Human) (DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE carboxypeptidase CPX-1))) (Fig. 15).

A multiple sequence alignment is given in FIG. 18, with the aortic carboxypeptidase-like proteins of the invention being shown in a ClustalW analysis comparing the proteins of the present invention with each other.

Accno	Common Name	Length
ACPL3	novel splice variant 2 of carboxypeptidase-like protein	202
ACPL1b	carboxypeptidase-like protein	734
ACPL2	novel splice variant 1 of carboxypeptidase-like protein	574

A search of the databases such as Pfam, PROSITE, ProDom, Blocks or Prints revealed the presence of identifiable domains in the ACPL3 polypeptide sequence as summarized in Table IV.

Table IV.

ACPL3

Model	Description	Score	E-value	N
F5_F8_type_C (InterPro)	F5/8 type C domain	-32.1	0.067	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
F5_F8_type_C	1/1	117	201 ..	1	158 []	-32.1	0.067

The domains identified in Table IV. are described as follows:

IPR000421 Coagulation factor 5/8 type C domain (FA58C): Blood coagulation factors V and VIII contain a C-terminal, twice repeated, domain of about 150 amino acids, which is called F5/8 type C, FA58C, or C1/C2- like domain. In the slime mold cell adhesion protein discoidin, a related domain, named discoidin I-like domain, DLD, or DS, has been found which shares a common C-terminal region of about 110 amino acids with the FA58C domain, but whose N-terminal 40 amino acids are much less conserved. Similar domains have been

detected in other extracellular and membrane proteins. In coagulation factors V and VIII the repeated domains compose part of a larger functional domain which promotes binding to anionic phospholipids on the surface of platelets and endothelial cells. The C-terminal domain of the second FA58C repeat (C2) of coagulation factor VIII has been shown to be responsible for phosphatidylserine-binding and essential for activity. It forms an amphipathic alpha-helix, which binds to the membrane. FA58C contains two conserved cysteines in most proteins, which link the extremities of the domain by a disulfide bond. A further disulfide bond is located near the C-terminal of the second FA58C domain in MFGM.

IPR000834 Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family: The carboxypeptidase A family (M14) can be divided into two subfamilies: carboxypeptidase H (regulatory) and carboxypeptidase A (digestive). Members of the H family have longer C-termini than those of family A, and carboxypeptidase M (a member of the H family) is bound to the membrane by a glycosylphosphatidylinositol anchor, unlike the majority of the M14 family, which are soluble. The zinc ligands have been determined as two histidines and a glutamate, and the catalytic residue has been identified as a C-terminal glutamate, but these do not form the characteristic metalloprotease HEXXH motif. Members of the carboxypeptidase A family are synthesised as inactive molecules with propeptides that must be cleaved to activate the enzyme. Structural studies of carboxypeptidases A and B reveal the polypeptide to exist as a globular domain, followed by an extended alpha-helix; this shields the catalytic site, without specifically binding to it, while the substrate-binding site is blocked by making specific contacts.

The novel nucleic acid of the invention encoding an aortic carboxypeptidase-like protein includes the proteins whose sequences are provided in Fig. 1, 8, 9, 11, and 13, or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in FIG. 1, 8, 9, 11, and 13, while still encoding a protein that maintains its aortic carboxypeptidase-like activities and physiological functions, or a fragment of such a nucleic acid. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

The invention further includes nucleic acids whose sequences are complementary to those just described. In the mutant or variant nucleic acid, up to 18% or more of the bases may be so changed.

The novel carboxypeptidase-like protein of the invention includes the proteins whose sequences is provided in FIG. 2, 10, and 12. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 2, 10 and 12 while still encoding a protein that maintains its aortic carboxypeptidase-like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to 18 % or more of the residues may be so changed.

For example, a variant of an ACPLX protein includes the a sequence of SEQ ID NO:2 in which the residue at position 192 is Arg and a residue at any other position may be altered, or in which the residue at position 387 is Arg and a residue at any other position may be altered. Alternateively, a variant of an ACPLX protein includes the a sequence of SEQ ID NO:2 in which the residue at position 192 is other than Ser and in which the residue at position 387 is other than Gln. Further a variant of an ACPLX protein includes the sequence in which at least one residue is altered from that of SEQ ID NO:2 by a permissive substitution. A a permissive substitution is one in which any amino acid residue that falls within a particular set of residues, defined in the following, may be substituted by any other amino acid residue of the same set. Since the side chains of many amino acid residues are structurally or functionally complex, a given amino acid may occur in more than one set. It is generally understood that a permissive substitution provides a variant whose structure and biological function are closely similar to the structure and biological function of the wild type prototype; in the present invention the wild type is considered to be the protein whose sequence of SEQ ID NO:2. The sets of permissive substitutions are:

[Gly, Ala, Pro];

[Ala, Val, Leu, Ile, Met, Phe, Tyr, Trp; Pro, Lys, Arg, Thr];

[Lys, Arg, His];

[Asp, Glu]; and

[Asn, Gln, Ser, Thr, Cys, His, Tyr, Trp, Asp, Glu, Lys, Arg]

In general, the substitutions leading to variants described above may be combined to provide polypeptides having a plurality of substitutions, as long as they conform to the guidelines set forth above. Any variant provided by the substitutions envisioned in this

invention retain structural and functional similarity to the wild type prototype polypeptide of SEQ ID NO:2. In addition, polypeptides that are mature forms of such variants, or fragments of such variants, are likewise encompassed within the present invention. Such mature forms and fragments retain structural and functional similarity to the wild type prototype polypeptide of SEQ ID NO:2. A variant of the complete polypeptide of SEQ ID NO:2, or a variant of a mature form thereof, or a variant of a fragment thereof, may have permissive substitutions in which any amino acid residue is changed to a different amino acid residue, provided that no more than 25%, or preferably no more than 20%, or more preferably no more than 15%, or more preferably no more than 10%, or more preferably no more than 5%, or more preferably no more than 3%, or still more preferably no more than 1%, of the amino acid residues in the sequence of the variant are so changed from the sequence provided by SEQ ID NO:2. In the case of fragments, the position of an amino acid residue is given by the position that the given residue would occupy if it were placed in its corresponding position in the full length polypeptide of SEQ ID NO:2.

Polypeptides similar to the polypeptides disclosed in the present invention have been described in U. S. Patent 6,140, 098, issued Oct. 31, 2000, PCT publication WO 01/10903, published February 15, 2001, and EP1074617, published February 7, 2001.

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

Based on sequence relatedness to known carboxypeptidase proteins as well as the the presence of identifiable domains, the present APCLX polypeptides may function as a binding protein that interacts with the cell surface mediating pro-hormone processing and/or interactions of hormones or other ligands with their receptors. For example, the AL035460A carboxypeptidase nucleic acid is differentially down regulated in certain cancers such as breast cancer and ovarian cancer. An expression analysis of this sequence is provided in the Examples. The AL035460A nucleic acid or protein may therefore be used as a differential diagnostic agent in distinguishing normal from cancerous tissues, and as a therapeutic agent in the treatment of cancers such as these.

The nucleic acids and proteins of the carboxypeptidase-like proteins and encoding nucleic acids of the invention are useful in potential therapeutic applications implicated in various hypertensive disorders and/or vascular endothelial disorders. Additional therapeutic applications are related to a putative prohormone processing function attributed to the protein. For example, a cDNA encoding the aortic carboxypeptidase-like protein may be useful in gene

therapy, and the aortic carboxypeptidase-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention have efficacy for treatment of patients suffering from hypertension, or atherosclerotic or comparable vascular pathologies. Additionally the compositions of the invention may be useful in treating conditions related to dysfunction in prohormone processing. The novel nucleic acid encoding aortic carboxypeptidase-like protein, and the protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

Gene mapping of AL035460 (APCL1) revealed the following diseases that map to the same location as the genomic sequence. It is therefore possible that the aortic carboxypeptidase-like gene product of AL035460A plays a role in one or more of the diseases Hallervorden-Spatz syndrome, Diabetes insipidus and/or tumor suppression in breast and ovarian cancer.

Hallervorden-Spatz syndrome (HSS) (OMIM #234200) is a rare, autosomal recessive neurodegenerative disorder with brain iron accumulation as a prominent finding. Clinical features include extrapyramidal dysfunction, onset in childhood, and a relentlessly progressive course. Histologic study reveals massive iron deposits in the basal ganglia. Systemic and cerebrospinal fluid iron levels are normal, as are plasma levels of ferritin, transferrin and ceruloplasmin. Conversely, in disorders of systemic iron overload, such as haemochromatosis, brain iron is not increased, which suggests that fundamental differences exist between brain and systemic iron metabolism and transport. In normal brain, non-haem iron accumulates regionally and is highest in basal ganglia. Pathologic brain iron accumulation is seen in common disorders, including Parkinson's disease, Alzheimer's disease and Huntington disease. In order to gain insight into normal and abnormal brain iron transport, metabolism and function, our approach was to map the gene for HSS. A primary genome scan was performed using samples from a large, consanguineous family (HS1). While this family was immensely powerful for mapping, the region demonstrating homozygosity in all affected members spans only 4 cM, requiring very close markers in order to detect linkage. The HSS gene maps to an interval flanked by D20S906 and D20S116 on chromosome 20p12.3-p13. Linkage was confirmed in nine additional families of diverse ethnic backgrounds.

With relation to diabetes insipidus, arginine vasopressin and its corresponding neurophysin are synthesized in the form of a common precursor which is cleaved by proteolysis to yield the biologically functional peptides (Sachs et al., Recent Prog. Horm. Res. 25: 447-491, 1969). Rats with hereditary diabetes insipidus are deficient in synthesis of both arginine vasopressin and one species of neurophysin (Sunde ET al. *Ann. N.Y. Acad. Sci.* 248: 345-364, 1975).

Both of the peptide hormones arginine vasopressin and oxytocin (OXT) are synthesized in the supraoptic nucleus (SON) and paraventricular nucleus (PVN) of the hypothalamus together with their respective 'carrier' proteins, the neurophysins (Brownstein, M. J.; Russell, J. T.; Gainer, H. Synthesis, transport, and release of posterior pituitary hormones. *Science* 207: 373-378, 1980).

Vasopressin and oxytocin are produced by separate populations of magnocellular neurons in both nuclei. Together with the neurophysins they are packaged into neurosecretory vesicles and transported axonally to the nerve endings in the neurohypophysis, where they are either stored or secreted into the bloodstream. Vasopressin is synthesized as a much larger precursor which includes—besides the hormone—its carrier protein, neurophysin, and a glycoprotein. The functional domains of the protein precursor are coded by 3 exons separated by 2 introns. The first exon encodes the hormone, the second most of the carrier protein, and the third the glycoprotein. A single nucleotide deletion is found in the second exon in the Brattleboro rat with diabetes insipidus (Schmale et al., EMBO J. 3: 3289-93, 1984). In addition, a single amino acid mutation in the binding protein for vasopressin (neuphysin) was discovered in human subjects with autosomal dominant neurohypophyseal diabetes insipidus (Repaske et al., J Clin Endocrinol Metab 79(2):421-7, 1994).

As noted, diabetes insipidus may be caused by mutations in the vasopressin-neurophysin precursor protein, resulting in improper targeting of the hormone to secretory vesicles. As a result the precursor protein accumulates in the endoplasmic reticulum and never reaches the Golgi for further processing (Olias et al., DNA Cell Biol.15: 929-935, 1996). The gene product from AL035460A may be involved in the processing and/or transport of the vasopressin-neurophysin pre-hormone product. Defects in the function of the gene product from an ALCLPLX gene, *e.g.*, AL035460A, may result in a defect in the production and secretion of active vasopressin, which may lead to the development of diabetes insipidus.

In relation to cancer, it is shown in the Examples that the AL035460A gene exhibits an expression profile consistent with it acting as a tumor suppressor gene in breast and ovarian

cancer (i.e., reduced expression in tumor cell lines relative to normal tissue). Thus, such tumor cells are predicted to exhibit a decrease in growth rate both *in vitro* and *in vivo* following transfection and expression of an ACPLX nucleic acid, *e.g.*, AL035460A.

ACPLX Nucleic Acids

The novel nucleic acids of the invention include those that encode an ACPLX polypeptide or protein. As used herein, the terms polypeptide and protein are interchangeable.

In some embodiments, an ALCPLX nucleic acid encodes a mature ACPLX polypeptide. As used herein, a "mature" form of a polypeptide or protein described herein relates to the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an open reading frame described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps that may take place within the cell in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an open reading frame, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

Among the ACPLX nucleic acids are the nucleic acids whose sequences are provided by SEQ ID NOS.: 1, 3, 4, 5, and 7, or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of SEQ ID NOS:1, 3, 4, 5, and 7, or a fragment thereof, any of whose bases may be changed from the corresponding bases shown in SEQ ID NOS:1, 3, 4, 5,

and 7 while still encoding a protein that maintains at least one of its ACPLX -like activities and physiological functions. The invention further includes the complements of the nucleic acid sequences of SEQ ID NO:1, 3, 4, 5, and 7 including fragments, derivatives, analogs and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

One aspect of the invention pertains to isolated nucleic acid molecules that encode ACPLX proteins or biologically active portions thereof. Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ACPLX-encoding nucleic acids (*e.g.*, ACPLX mRNA) and fragments for use as polymerase chain reaction (PCR) primers for the amplification or mutation of ACPLX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated ACPLX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of

other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having any of the nucleotide sequences of SEQ ID NOS:1, 3, 4, 5, or 7, or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequences of SEQ ID NOS:1, 3, 4, 5 or 7 as a hybridization probe, ACPLX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ACPLX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at lease 6 contiguous nucleotides of any one of SEQ ID NOS:1, 3, 4, 5 or 7, or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, isolated nucleic acid molecules of the invention include nucleic acid molecules that are complements of the nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 5, and 7. In another embodiment, isolated nucleic acid molecules of the invention comprise nucleic acid molecules that are complements of the nucleotide sequence shown in SEQ ID NOS:1, 3, 4, 5, and 7, or a portion of this nucleotide sequence. A nucleic

acid molecule that is complementary to the nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 5, and 7 is one that is sufficiently complementary to the nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 5, and 7 that it can hydrogen bond with little or no mismatches to the nucleotide sequences shown in SEQ ID NO:1, 3, 4, 5, and 7, thereby forming a stable duplex.

As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Moreover, the nucleic acid molecules of the invention can comprise only a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 4, 5, and 7, *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ACPLX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or

amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ACPLX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for ACPLX polypeptides of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ACPLX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NO:2, as well as a polypeptide having ACPLX activity. Biological activities of the ACPLX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ACPLX polypeptide.

The nucleotide sequence determined from the cloning of the human ACPLX gene allows for the generation of probes and primers designed for use in identifying and/or cloning ACPLX homologues in other cell types, *e.g.*, from other tissues, as well as ACPLX homologues from other mammals. The probe/primer typically comprises a substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200,

250, 300, 350 or 400 or more consecutive sense strand nucleotide sequences of SEQ ID NOS:1, 3, 4, 5, and 7; or an anti-sense strand nucleotide sequences of SEQ ID NOS:1, 3, 4, 5, and 7; or of a naturally occurring mutant of SEQ ID NOS:1, 3, 4, 5, and 7.

Probes based on the human ACPLX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress an ACPLX protein, such as by measuring a level of an ACPLX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ACPLX mRNA levels or determining whether a genomic ACPLX gene has been mutated or deleted.

A "polypeptide having a biologically active portion of ACPLX" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ACPLX" can be prepared by isolating a portion of any of SEQ ID NOS:1, 3, 4, 5, or 7 that encodes a polypeptide having an ACPLX biological activity (biological activities of the ACPLX proteins are described below), expressing the encoded portion of ACPLX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ACPLX. For example, a nucleic acid fragment encoding a biologically active portion of ACPLX can optionally include an ATP-binding domain. In another embodiment, a nucleic acid fragment encoding a biologically active portion of ACPLX includes one or more regions.

ACPLX Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 5, and 7 due to the degeneracy of the genetic code. These nucleic acids thus encode the same ACPLX proteins as that encoded by the nucleotide sequence shown in SEQ ID NOS:1, 3, 4, 5, and 7, *e.g.*, the polypeptides of SEQ ID NOS:2, 6, and 8. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS:2, 6, and 8.

In addition to the human ACPLX nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 5, and 7, it will be appreciated by those skilled in the art that DNA sequence polymorphisms

that lead to changes in the amino acid sequences of ACPLX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ACPLX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an ACPLX protein, preferably a mammalian ACPLX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ACPLX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ACPLX that are the result of natural allelic variation and that do not alter the functional activity of ACPLX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ACPLX proteins from other species, and thus that have nucleotide sequences that differ from the human sequences of SEQ ID NOS:1, 3, 4, 5, and 7 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ACPLX cDNAs of the invention can be isolated based on their homology to the human ACPLX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. For example, a soluble human ACPLX cDNA can be isolated based on its homology to human membrane-bound ACPLX. Likewise, a membrane-bound human ACPLX cDNA can be isolated based on its homology to soluble human ACPLX.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecules comprising the nucleotide sequences of SEQ ID NOS:1,3 , 4, 5, and 7. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ACPLX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at Tm, 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:1 corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecules comprising the nucleotide sequences of SEQ ID NOS:1, 3, 4, 5, and 7, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of

moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecules comprising the nucleotide sequences of SEQ ID NOS:1, 3, 4, 5, and 7, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA 78*: 6789-6792.

Conservative mutations

In addition to naturally-occurring allelic variants of the ACPLX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences of SEQ ID NOS:1, 3, 4, 5, and 7, thereby leading to changes in the amino acid sequence of the encoded ACPLX protein, without altering the functional ability of the ACPLX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequences of SEQ ID NOS:1, 3, 4, 5, and 7. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ACPLX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ACPLX proteins of the present invention, are predicted to be particularly unamenable to alteration.

In addition, amino acid residues that are conserved among ACPLX members, as indicated by the alignments presented in FIGS. 3 and 4, are predicted to be less amenable to alteration. For example, ACPLX proteins of the present invention can contain at least one domain that is a typically conserved region in ACPLX members, *i.e.* carboxypeptidase family

proteins, and ACPLX homologs. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.* those that are not conserved or only semi-conserved among the members of the ACPLX proteins) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ACPLX proteins that contain changes in amino acid residues that are not essential for activity. Such ACPLX proteins differ in amino acid sequence from SEQ ID NOS:2, 6, and 8 yet retain biological activity. In one embodiment, the isolated nucleic acid molecules comprise a nucleotide sequence encoding a proteins, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequences of SEQ ID NOS:2, 6, and 8. Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to SEQ ID NOS:2, 6, and 8, more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NOS:2, 6, and 8.

An isolated nucleic acid molecule encoding an ACPLX protein homologous to the proteins of SEQ ID NOS:2, 6, and 8 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NOS:1, 3, 4, 5, and 7, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into the nucleotide sequences of SEQ ID NOS:1,3 ,4 , 5, and 7 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ACPLX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an ACPLX coding sequence, such as by saturation mutagenesis, and the resultant

mutants can be screened for ACPLX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NOS:1, 3, 4, 5, or 7, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ACPLX protein can be assayed for (1) the ability to form protein:protein interactions with other ACPLX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ACPLX protein and an ACPLX receptor; (3) the ability of a mutant ACPLX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ACPLX protein antibody.

Antisense ACPLX Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequences of SEQ ID NOS:1, 3, 4, 5, and 7, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ACPLX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of ACPLX proteins of SEQ ID NOS:2, 6, and 8, or antisense nucleic acids complementary to ACPLX nucleic acid sequences of SEQ ID NOS:1, 3, 4, 5, and 7 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ACPLX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the protein coding region of human ACPLX corresponds to SEQ ID NOS:2, 6, and 8). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ACPLX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ACPLX disclosed herein (*e.g.*, SEQ ID NOS:1, 3, 4, 5, and 7), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ACPLX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ACPLX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ACPLX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or

genomic DNA encoding an ACPLX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

ACPLX Ribozymes and PNA moieties

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave

ACPLX mRNA transcripts to thereby inhibit translation of ACPLX mRNA. A ribozyme having specificity for an ACPLX-encoding nucleic acid can be designed based upon the nucleotide sequence of an ACPLX DNA disclosed herein (*i.e.*, SEQ ID NOS:1, 3, 4, 5, and 7). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an ACPLX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, ACPLX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, ACPLX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ACPLX (*e.g.*, the ACPLX promoter and/or enhancers) to form triple helical structures that prevent transcription of the ACPLX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of ACPLX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ACPLX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ACPLX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ACPLX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ACPLX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, Proc. *Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ACPLX polypeptides

An ACPLX polypeptide of the invention includes the ACPLX-like protein whose sequences are provided in SEQ ID NOS:2, 6, and 8. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in SEQ ID NOS:2, 6, and 8 while still encoding a protein that maintains its ACPLX-like activities and physiological functions, or a functional fragment thereof. In some embodiments, up to 20% or more of the residues may be so changed in the mutant or variant protein. In some embodiments, the ACPLX polypeptide according to the invention is a mature polypeptide.

In general, an ACPLX -like variant that preserves ACPLX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated ACPLX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ACPLX antibodies. In one embodiment, native ACPLX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ACPLX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an ACPLX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ACPLX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ACPLX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ACPLX protein having less than about 30% (by dry weight) of non-ACPLX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of

non-ACPLX protein, still more preferably less than about 10% of non-ACPLX protein, and most preferably less than about 5% non-ACPLX protein. When the ACPLX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ACPLX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ACPLX protein having less than about 30% (by dry weight) of chemical precursors or non-ACPLX chemicals, more preferably less than about 20% chemical precursors or non-ACPLX chemicals, still more preferably less than about 10% chemical precursors or non-ACPLX chemicals, and most preferably less than about 5% chemical precursors or non-ACPLX chemicals.

Biologically active portions of an ACPLX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ACPLX protein, *e.g.*, the amino acid sequences shown in SEQ ID NOS:2, 6, and 8 that include fewer amino acids than the full length ACPLX proteins, and exhibit at least one activity of an ACPLX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ACPLX protein. A biologically active portion of an ACPLX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of an ACPLX protein of the present invention may contain at least one of the above-identified domains conserved between the ACPLX proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ACPLX protein.

In an embodiment, the ACPLX protein has an amino acid sequence shown in any of SEQ ID NOS:2, 6, and 8. In other embodiments, the ACPLX protein is substantially homologous to any of SEQ ID NOS:2, 6, and 8, and retains the functional activity of the proteins of SEQ ID NOS:2, 6, and 8, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ACPLX protein is a protein that comprises an amino acid sequence at least about 45%

homologous to the amino acid sequences of SEQ ID NOS:2, 6, and 8 and retains the functional activity of the ACPLX proteins of SEQ ID NOS:2, 6, and 8.

Determining homology between two or more sequence

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch* 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequences shown in SEQ ID NOS:1, 3, 4, 5, and 7.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a

reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.,* the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ACPLX chimeric or fusion proteins. As used herein, an ACPLX "chimeric protein" or "fusion protein" comprises an ACPLX polypeptide operatively linked to a non-ACPLX polypeptide. An "ACPLX polypeptide" refers to a polypeptide having an amino acid sequences corresponding to ACPLX proteins (SEQ ID NOS:2, 6, and 8), whereas a "non-ACPLX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ACPLX protein, *e.g.*, a protein that is different from the ACPLX protein and that is derived from the same or a different organism. Within an ACPLX fusion protein the ACPLX polypeptide can correspond to all or a portion of an ACPLX protein. In one embodiment, an ACPLX fusion protein comprises at least one biologically active portion of an ACPLX protein. In another embodiment, an ACPLX fusion protein comprises at least two biologically active portions of an ACPLX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ACPLX polypeptide and the non-ACPLX polypeptide are fused in-frame to each other. The non-ACPLX polypeptide can be fused to the N-terminus or C-terminus of the ACPLX polypeptide.

For example, in one embodiment an ACPLX fusion protein comprises an ACPLX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ACPLX activity (such assays are described in detail below).

Alternatively, the second polypeptide can be fused to either the amino-terminus or carboxyl-terminus of CG54007-04 and CG54007-05 polypeptides. Futher, a third nonhomologous polypeptide or protein may also be fused to the novel splice variant of carboxypeptidase-like protein such that the second nonhomologous polypeptide or protein is joined at the amino terminus, and the third nonhomologous polypeptide or protein is joined at

the carboxyl terminus, of the CG54007-04 and CG54007-05 polypeptides. Examples of nonhomologous sequences that may be incorporated as either a second or third polypeptide or protein include glutathione S-transferase, a heterologous signal sequence fused at the amino terminus of the splice variant of carboxypeptidase-like protein, an immunoglobulin sequence or domain, a serum protein or domain thereof (such as a serum albumin), an antigenic epitope, and a specificity motif such as $(His)_6$.

In another embodiment, the fusion protein is a GST-ACPLX fusion protein in which the ACPLX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ACPLX.

In yet another embodiment, the fusion protein is an ACPLX protein containing a heterologous signal sequence at its N-terminus. For example, the native ACPLX signal sequence (*i.e.*, amino acids 20 to 21 of SEQ ID NO:2) can be removed and replaced with a signal sequence from another protein. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of ACPLX can be increased through use of a heterologous signal sequence.

In another embodiment, the fusion protein is an ACPLX-immunoglobulin fusion protein in which the ACPLX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ACPLX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an ACPLX ligand and an ACPLX protein on the surface of a cell, to thereby suppress ACPLX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ACPLX ligand of the invention is the ACPLX receptor. The ACPLX-immunoglobulin fusion proteins can be used to affect the bioavailability of an ACPLX cognate ligand. Inhibition of the ACPLX ligand/ACPLX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the ACPLX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ACPLX antibodies in a subject, to purify ACPLX ligands, and in screening assays to identify molecules that inhibit the interaction of ACPLX with an ACPLX ligand.

An ACPLX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional

techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An ACPLX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ACPLX protein.

ACPLX agonists and antagonists

The present invention also pertains to variants of the ACPLX proteins that function as either ACPLX agonists (mimetics) or as ACPLX antagonists. Variants of the ACPLX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ACPLX protein. An agonist of the ACPLX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ACPLX protein. An antagonist of the ACPLX protein can inhibit one or more of the activities of the naturally occurring form of the ACPLX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ACPLX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ACPLX proteins.

Variants of the ACPLX protein that function as either ACPLX agonists (mimetics) or as ACPLX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ACPLX protein for ACPLX protein agonist or antagonist activity. In one embodiment, a variegated library of ACPLX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ACPLX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of

potential ACPLX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ACPLX sequences therein. There are a variety of methods which can be used to produce libraries of potential ACPLX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ACPLX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

Polypeptide libraries

In addition, libraries of fragments of the ACPLX protein coding sequence can be used to generate a variegated population of ACPLX fragments for screening and subsequent selection of variants of an ACPLX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an ACPLX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ACPLX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ACPLX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recrusive ensemble

mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ACPLX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

ACPLX Antibodies

Also included in the invention are antibodies to ACPLX proteins, or fragments of ACPLX proteins. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated ACPLX-related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in any of SEQ ID NO:2, 6, or 8, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of ACPLX-related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human ACPLX-related protein sequence will indicate which regions of an ACPLX-related protein are particularly

hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents.

Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are

employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically

two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's

endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse™ as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that

binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion

preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in

vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain

(from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

ACPLX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an ACPLX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*,

non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to includes promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, ACPLX proteins, mutant forms of ACPLX proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ACPLX proteins in prokaryotic or eukaryotic cells. For example, ACPLX proteins can be

expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (*i*) to increase expression of recombinant protein; (*ii*) to increase the solubility of the recombinant protein; and (*iii*) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. *See, e.g.,* Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (*see, e.g.,* Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ACPLX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerivisae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, ACPLX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, *e.g.*, Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also

encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α-fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ACPLX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.,* Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ACPLX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or

electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ACPLX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ACPLX protein. Accordingly, the invention further provides methods for producing ACPLX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ACPLX protein has been introduced) in a suitable medium such that ACPLX protein is produced. In another embodiment, the method further comprises isolating ACPLX protein from the medium or the host cell.

Transgenic ACPLX Animals

The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ACPLX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ACPLX sequences have been introduced into their genome or homologous recombinant animals in which endogenous ACPLX sequences have been altered. Such animals are useful for studying the function and/or activity of ACPLX protein and for identifying and/or evaluating modulators of ACPLX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of

transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ACPLX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ACPLX-encoding nucleic acid into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. Sequences including SEQ ID NOS:1, 3, 4, 5, and 7 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human ACPLX gene, such as a mouse ACPLX gene, can be isolated based on hybridization to the human ACPLX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the ACPLX transgene to direct expression of ACPLX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ACPLX transgene in its genome and/or expression of ACPLX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding ACPLX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an ACPLX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ACPLX gene. The ACPLX gene can

be a human gene (*e.g.*, the DNA of SEQ ID NOS:1, 3, 4, 5, and 7), but more preferably, is a non-human homologue of a human ACPLX gene. For example, a mouse homologue of human ACPLX gene of SEQ ID NOS:1, 3, 4, 5, or 7 can be used to construct a homologous recombination vector suitable for altering an endogenous ACPLX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ACPLX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ACPLX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ACPLX protein). In the homologous recombination vector, the altered portion of the ACPLX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the ACPLX gene to allow for homologous recombination to occur between the exogenous ACPLX gene carried by the vector and an endogenous ACPLX gene in an embryonic stem cell. The additional flanking ACPLX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g.,* Thomas, *et al.*, 1987. *Cell* 51: 503 for a description of homologous recombination vectors. The vector is ten introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced ACPLX gene has homologously-recombined with the endogenous ACPLX gene are selected. *See, e.g.*, Li, *et al.*, 1992. *Cell* 69: 915.

The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras. *See, e.g.*, Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, 1991. *Curr. Opin. Biotechnol.* 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, *See, e.g.*, Lakso, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae. See,* O'Gorman, *et al.*, 1991. *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, *et al.*, 1997. *Nature* 385: 810-813. In brief, a cell (*e.g.*, a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (*e.g.*, the somatic cell) is isolated.

Pharmaceutical Compositions

The ACPLX nucleic acid molecules, ACPLX proteins, and anti-ACPLX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5%

human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The antibodies disclosed herein can also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang et al., Proc. Natl Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al ., J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., J. National Cancer Inst., 81(19): 1484 (1989).

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.,* topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an ACPLX protein or anti-ACPLX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier

for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared

according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.,* U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

Antibodies specifically binding a protein of the invention, as well as other molecules identified by the screening assays disclosed herein, can be administered for the treatment of various disorders in the form of pharmaceutical compositions. Principles and considerations involved in preparing such compositions, as well as guidance in the choice of components are provided, for example, in Remington : The Science And Practice Of Pharmacy 19th ed. (Alfonso R. Gennaro, et al., editors) Mack Pub. Co., Easton, Pa. : 1995; Drug Absorption Enhancement : Concepts, Possibilities, Limitations, And Trends, Harwood Academic Publishers, Langhorne, Pa., 1994; and Peptide And Protein Drug Delivery (Advances In Parenteral Sciences, Vol. 4), 1991, M. Dekker, New York. If the antigenic protein is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically

binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, 1993 *Proc. Natl. Acad. Sci. USA*, 90: 7889-7893. The formulation herein can also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition can comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.The active ingredients can also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions.

The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations can be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT ™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express ACPLX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ACPLX mRNA (*e.g.*, in a biological sample) or a genetic lesion in an ACPLX gene, and to modulate ACPLX activity, as described further, below. In addition, the ACPLX proteins can be used to screen drugs or compounds that modulate the ACPLX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of ACPLX protein or production of ACPLX protein forms that have decreased or aberrant activity compared to ACPLX wild-type protein (*e.g.* Anxiety disorders; CNS disorders where GABA neurotransmitters are involved; Diabetes (regulates insulin release); Obesity (binds and transport lipids); and Infectious Disease(possesses anti-microbial activity). In addition, the anti-ACPLX antibodies of the invention can be used to detect and isolate ACPLX proteins and modulate ACPLX activity.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra.*

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to ACPLX proteins or have a stimulatory or inhibitory effect on, *e.g.,* ACPLX protein expression or ACPLX protein activity. The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an ACPLX protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. *See, e.g.,* Lam, 1997. *Anticancer Drug Design* 12: 145.

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, *e.g.*, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*, 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2059; Carell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ACPLX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an ACPLX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ACPLX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ACPLX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the

assay comprises contacting a cell which expresses a membrane-bound form of ACPLX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds ACPLX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an ACPLX protein, wherein determining the ability of the test compound to interact with an ACPLX protein comprises determining the ability of the test compound to preferentially bind to ACPLX protein or a biologically-active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ACPLX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ACPLX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of ACPLX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the ACPLX protein to bind to or interact with an ACPLX target molecule. As used herein, a "target molecule" is a molecule with which an ACPLX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an ACPLX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An ACPLX target molecule can be a non-ACPLX molecule or an ACPLX protein or polypeptide of the invention. In one embodiment, an ACPLX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound ACPLX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ACPLX.

Determining the ability of the ACPLX protein to bind to or interact with an ACPLX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ACPLX protein to bind to or interact with an ACPLX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+}, diacylglycerol, IP_3, etc.), detecting catalytic/enzymatic activity of the target an appropriate

substrate, detecting the induction of a reporter gene (comprising an ACPLX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an ACPLX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the ACPLX protein or biologically-active portion thereof. Binding of the test compound to the ACPLX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the ACPLX protein or biologically-active portion thereof with a known compound which binds ACPLX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an ACPLX protein, wherein determining the ability of the test compound to interact with an ACPLX protein comprises determining the ability of the test compound to preferentially bind to ACPLX or biologically-active portion thereof as compared to the known compound.

In still another embodiment, an assay is a cell-free assay comprising contacting ACPLX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the ACPLX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of ACPLX can be accomplished, for example, by determining the ability of the ACPLX protein to bind to an ACPLX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ACPLX protein can be accomplished by determining the ability of the ACPLX protein further modulate an ACPLX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described above.

In yet another embodiment, the cell-free assay comprises contacting the ACPLX protein or biologically-active portion thereof with a known compound which binds ACPLX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an ACPLX protein, wherein determining the ability of the test compound to interact with an ACPLX protein comprises

determining the ability of the ACPLX protein to preferentially bind to or modulate the activity of an ACPLX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of ACPLX protein. In the case of cell-free assays comprising the membrane-bound form of ACPLX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ACPLX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either ACPLX protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ACPLX protein, or interaction of ACPLX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-ACPLX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ACPLX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes can be dissociated from the matrix, and the level of ACPLX protein binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the ACPLX protein or its target

molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ACPLX protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well-known within the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ACPLX protein or target molecules, but which do not interfere with binding of the ACPLX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ACPLX protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ACPLX protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ACPLX protein or target molecule.

In another embodiment, modulators of ACPLX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ACPLX mRNA or protein in the cell is determined. The level of expression of ACPLX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ACPLX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ACPLX mRNA or protein expression based upon this comparison. For example, when expression of ACPLX mRNA or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ACPLX mRNA or protein expression. Alternatively, when expression of ACPLX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of ACPLX mRNA or protein expression. The level of ACPLX mRNA or protein expression in the cells can be determined by methods described herein for detecting ACPLX mRNA or protein.

In yet another aspect of the invention, the ACPLX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054; Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with ACPLX ("ACPLX-binding proteins" or "ACPLX-bp") and modulate ACPLX activity. Such

ACPLX-binding proteins are also likely to be involved in the propagation of signals by the ACPLX proteins as, for example, upstream or downstream elements of the ACPLX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ACPLX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an ACPLX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ACPLX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (*i*) identify an individual from a minute biological sample (tissue typing); and (*ii*) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

Tissue Typing

The ACPLX sequences of the invention can be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an

individual's genome. Thus, the ACPLX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The ACPLX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS:1, 3, 5, or 7 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining ACPLX protein and/or nucleic acid expression as well as ACPLX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ACPLX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ACPLX protein, nucleic acid expression or activity. For example, mutations in an ACPLX gene can be

assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ACPLX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining ACPLX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ACPLX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of ACPLX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ACPLX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ACPLX protein such that the presence of ACPLX is detected in the biological sample. An agent for detecting ACPLX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ACPLX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length ACPLX nucleic acid, such as the nucleic acids of SEQ ID NOS:1, 3, 4, 5, and 7, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ACPLX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

One agent for detecting ACPLX protein is an antibody capable of binding to ACPLX protein, preferably an antibody with a detectable label. Antibodies directed against a protein of the invention may be used in methods known within the art relating to the localization and/or quantitation of the protein (e.g., for use in measuring levels of the protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies against the proteins, or derivatives,

fragments, analogs or homologs thereof, that contain the antigen binding domain, are utilized as pharmacologically-active compounds.

An antibody specific for a protein of the invention can be used to isolate the protein by standard techniques, such as immunoaffinity chromatography or immunoprecipitation. Such an antibody can facilitate the purification of the natural protein antigen from cells and of recombinantly produced antigen expressed in host cells. Moreover, such an antibody can be used to detect the antigenic protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the antigenic protein. Antibodies directed against the protein can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ACPLX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of ACPLX mRNA include

Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ACPLX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of ACPLX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ACPLX protein include introducing into a subject a labeled anti-ACPLX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In one embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ACPLX protein, mRNA, or genomic DNA, such that the presence of ACPLX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ACPLX protein, mRNA or genomic DNA in the control sample with the presence of ACPLX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ACPLX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ACPLX protein or mRNA in a biological sample; means for determining the amount of ACPLX in the sample; and means for comparing the amount of ACPLX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ACPLX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ACPLX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ACPLX protein, nucleic acid expression or activity. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a

disease or disorder associated with aberrant ACPLX expression or activity in which a test sample is obtained from a subject and ACPLX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ACPLX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ACPLX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant ACPLX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ACPLX expression or activity in which a test sample is obtained and ACPLX protein or nucleic acid is detected (*e.g.*, wherein the presence of ACPLX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ACPLX expression or activity).

The methods of the invention can also be used to detect genetic lesions in an ACPLX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an ACPLX-protein, or the misexpression of the ACPLX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (*i*) a deletion of one or more nucleotides from an ACPLX gene; (*ii*) an addition of one or more nucleotides to an ACPLX gene; (*iii*) a substitution of one or more nucleotides of an ACPLX gene, (*iv*) a chromosomal rearrangement of an ACPLX gene; (*v*) an alteration in the level of a messenger RNA transcript of an ACPLX gene, (*vi*) aberrant modification of an ACPLX gene, such as of the methylation pattern of the genomic DNA, (*vii*) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an ACPLX gene, (*viii*) a non-wild-type level of an ACPLX protein, (*ix*) allelic loss of an ACPLX gene, and (*x*) inappropriate post-translational

modification of an ACPLX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an ACPLX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.*, U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.*, Landegran, *et al.*, 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for detecting point mutations in the ACPLX-gene (*see,* Abravaya, *et al.*, 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an ACPLX gene under conditions such that hybridization and amplification of the ACPLX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (*see,* Guatelli, *et al.*, 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see,* Kwoh, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177); Qβ Replicase (*see,* Lizardi, *et al*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an ACPLX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent

No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ACPLX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes. *See, e.g.,* Cronin, *et al.*, 1996. *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic mutations in ACPLX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra.* Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ACPLX gene and detect mutations by comparing the sequence of the sample ACPLX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (*see, e.g.,* Naeve, *et al.*, 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publication No. WO 94/16101; Cohen, *et al.*, 1996. *Adv. Chromatography* 36: 127-162; and Griffin, *et al.*, 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the ACPLX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. *See, e.g.,* Myers, *et al.*, 1985. *Science* 230: 1242. In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ACPLX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as

which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S_1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. *See, e.g.,* Cotton, *et al.,* 1988. *Proc. Natl. Acad. Sci. USA* 85: 4397; Saleeba, *et al.,* 1992. *Methods Enzymol.* 217: 286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ACPLX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. *See, e.g.,* Hsu, *et al.,* 1994. *Carcinogenesis* 15: 1657-1662. According to an exemplary embodiment, a probe based on an ACPLX sequence, *e.g.*, a wild-type ACPLX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. *See, e.g.,* U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ACPLX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. *See, e.g.,* Orita, *et al.,* 1989. *Proc. Natl. Acad. Sci. USA*: 86: 2766; Cotton, 1993. *Mutat. Res.* 285: 125-144; Hayashi, 1992. *Genet. Anal. Tech. Appl.* 9: 73-79. Single-stranded DNA fragments of sample and control ACPLX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded

heteroduplex molecules on the basis of changes in electrophoretic mobility. *See, e.g.,* Keen, *et al.*, 1991. *Trends Genet.* 7: 5.

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). *See, e.g.,* Myers, *et al.,* 1985. *Nature* 313: 495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. *See, e.g.,* Rosenbaum and Reissner, 1987. *Biophys. Chem.* 265: 12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g.,* Saiki, *et al.*, 1986. *Nature* 324: 163; Saiki, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization; *see, e.g.,* Gibbs, *et al.*, 1989. *Nucl. Acids Res.* 17: 2437-2448) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g.,* Prossner, 1993. *Tibtech.* 11: 238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. *See, e.g.,* Gasparini, *et al.,* 1992. *Mol. Cell Probes* 6: 1. It is anticipated that in certain embodiments amplification may also be performed using *Taq* ligase for amplification. *See, e.g.,* Barany, 1991. *Proc. Natl. Acad. Sci. USA* 88: 189. In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an ACPLX gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ACPLX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on ACPLX activity (*e.g.*, ACPLX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, cancer or immune disorders associated with aberrant ACPLX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of ACPLX protein, expression of ACPLX nucleic acid, or mutation content of ACPLX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can

occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ACPLX protein, expression of ACPLX nucleic acid, or mutation content of ACPLX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an ACPLX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ACPLX (*e.g.*, the ability to modulate aberrant cell proliferation and/or

differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ACPLX gene expression, protein levels, or upregulate ACPLX activity, can be monitored in clinical trails of subjects exhibiting decreased ACPLX gene expression, protein levels, or downregulated ACPLX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease ACPLX gene expression, protein levels, or downregulate ACPLX activity, can be monitored in clinical trails of subjects exhibiting increased ACPLX gene expression, protein levels, or upregulated ACPLX activity. In such clinical trials, the expression or activity of ACPLX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

By way of example, and not of limitation, genes, including ACPLX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ACPLX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ACPLX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ACPLX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a subject prior to administration of the agent; (*ii*) detecting the level of expression of an ACPLX protein, mRNA, or genomic DNA in the preadministration sample; (*iii*) obtaining one or more post-administration samples from the subject; (*iv*) detecting the level of expression or activity of the ACPLX protein, mRNA, or genomic DNA in the post-administration samples; (*v*) comparing the level of expression or activity of the ACPLX

protein, mRNA, or genomic DNA in the pre-administration sample with the ACPLX protein, mRNA, or genomic DNA in the post administration sample or samples; and (*vi*) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ACPLX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ACPLX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ACPLX expression or activity. These methods of treatment will be discussed more fully, below.

Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (*i*) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (*ii*) antibodies to an aforementioned peptide; (*iii*) nucleic acids encoding an aforementioned peptide; (*iv*) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endoggenous function of an aforementioned peptide by homologous recombination (*see, e.g.*, Capecchi, 1989. *Science* 244: 1288-1292); or (*v*) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be

utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.,* from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.,* by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.,* Northern assays, dot blots, *in situ* hybridization, and the like).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ACPLX expression or activity, by administering to the subject an agent that modulates ACPLX expression or at least one ACPLX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ACPLX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ACPLX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of ACPLX aberrancy, for example, an ACPLX agonist or ACPLX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

Therapeutic Methods

Another aspect of the invention pertains to methods of modulating ACPLX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ACPLX protein activity associated with the cell. An agent that modulates ACPLX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of an ACPLX protein, a peptide, an ACPLX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ACPLX protein activity. Examples of

such stimulatory agents include active ACPLX protein and a nucleic acid molecule encoding ACPLX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ACPLX protein activity. Examples of such inhibitory agents include antisense ACPLX nucleic acid molecules and anti-ACPLX antibodies. These modulatory methods can be performed *in vitro* (*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an ACPLX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, up-regulates or down-regulates) ACPLX expression or activity. In another embodiment, the method involves administering an ACPLX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ACPLX expression or activity.

Stimulation of ACPLX activity is desirable in situations in which ACPLX is abnormally downregulated and/or in which increased ACPLX activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (*e.g.*, cancer or immune associated disorders). Another example of such a situation is where the subject has a gestational disease (*e.g.*, preclampsia).

Antibodies of the invention, including polyclonal, monoclonal, humanized and fully human antibodies, may used as therapeutic agents. Such agents will generally be employed to treat or prevent a disease or pathology in a subject. An antibody preparation, preferably one having high specificity and high affinity for its target antigen, is administered to the subject and will generally have an effect due to its binding with the target. Such an effect may be one of two kinds, depending on the specific nature of the interaction between the given antibody molecule and the target antigen in question. In the first instance, administration of the antibody may abrogate or inhibit the binding of the target with an endogenous ligand to which it naturally binds. In this case, the antibody binds to the target and masks a binding site of the naturally occurring ligand, wherein the ligand serves as an effector molecule. Thus the receptor mediates a signal transduction pathway for which ligand is responsible.

Alternatively, the effect may be one in which the antibody elicits a physiological result by virtue of binding to an effector binding site on the target molecule. In this case the target, a receptor having an endogenous ligand which may be absent or defective in the disease or

pathology, binds the antibody as a surrogate effector ligand, initiating a receptor-based signal transduction event by the receptor.

A therapeutically effective amount of an antibody of the invention relates generally to the amount needed to achieve a therapeutic objective. As noted above, this may be a binding interaction between the antibody and its target antigen that, in certain cases, interferes with the functioning of the target, and in other cases, promotes a physiological response. The amount required to be administered will furthermore depend on the binding affinity of the antibody for its specific antigen, and will also depend on the rate at which an administered antibody is depleted from the free volume other subject to which it is administered. Common ranges for therapeutically effective dosing of an antibody or antibody fragment of the invention may be, by way of nonlimiting example, from about 0.1 mg/kg body weight to about 50 mg/kg body weight. Common dosing frequencies may range, for example, from twice daily to once a week.

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Determination of the Biological Effect of the Therapeutic

In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

The invention will be further illustrated using the following non-limiting examples.

Example 1. Molecular cloning of an ACPL1a nucleic acid ("AL035460A")

A nucleotide sequence (SEQ ID NO:1) shown in FIG.1 encoding a polypeptide (SEQ ID NO:2) related to known carboxypeptideases was identified by assembling various regions of human genomic DNA. The assembled sequence was named AL035460A (ACPL1a).

The SIGNALP secretory signal prediction algorithm predicts that the polypeptide (SEQ IDNO:2) encoded by AL035460A has a signal peptidase cleavage site between residues 20 and 21. Accordingly the predicted ORF corresponding to the mature form of the encoded AL035460A protein was cloned.

Oligonucleotide primers were designed to amplify the DNA segment corresponding to this protein using PCR. The forward primer included an in frame BglII restriction site, and the reverse primer contained an in frame XhoI restriction site. The following PCR primers were used:

AL035460A Forw:

CTCGTCAGATCTGCGCCCAGGAACTCGGTGCTGGGCCTCG (SEQ ID NO:14),

and

AL035460A Rev:

CTCGTCCTCGAGATCCTTCTGTCCCCTTAGCCGCTCC (SEQ ID NO:15).

PCR reactions were performed using a total of 5ng human adult heart cDNA template, 1 microM of each of the AL035460A Forw and AL035460A Rev primers, 5 micromoles dNTP (Clontech Laboratories, Palo Alto CA) and 1 microliter of 50xAdvantage-HF 2 polymerase (Clontech Laboratories, Palo Alto CA) in 50 microliter volume. The following reaction conditions were used:

a) 96°C 3 minutes

b) 96°C 30 seconds denaturation

c) 70°C 30 seconds, primer annealing.

d) 72°C 4 minute extension.

Repeat steps b-d 10 times, decreasing the temperature of step c) by 1°C/cycle;

e) 96°C 30 seconds denaturation

f) 60°C 30 seconds annealing

g) 72°C 4 minute extension

Repeat steps e-g 25 times;

h) 72°C 10 minutes final extension.

A PCR product having the expected size, approximately 2.2 kbp, was isolated from an agarose gel and ligated to the vector pCR2.1 (Invitrogen, Carlsbad, CA). The cloned insert

was sequenced using vector specific, M13 Forward(-40) and M13 Reverse primers, as well as the following gene specific primers:

AL035460A S1:	AGCCGGCTTGAGGCATCCAGC	(SEQ ID NO:16),
AL035460A S2:	GCTGGATGCCTCAAGCCGGCT	(SEQ ID NO:17),
AL035460A S3:	CCAGAAACTCCAGTGCTGAAC	(SEQ ID NO:18),
AL035460A S4:	GTTCAGCACTGGAGTTTCTGG	(SEQ ID NO:19),
AL035460A S5:	CAAGCCTGGGGAGCATGAGCTG	(SEQ ID NO:20),
AL035460A S6:	CAGCTCATGCTCCCCAGGCTTG	(SEQ ID NO:21),
AL035460A S7:	CAGGACGATGGGAAGGTGCCC	(SEQ ID NO:22),
AL035460A S8:	GGGCACCTTCCCATCGTCCTG	(SEQ ID NO:23),
AL035460A S9:	AGCATGAATGACTTCAGCTAC	(SEQ ID NO:24),
AL035460A S10:	GTAGCTGAAGTCATTCATGCT	(SEQ ID NO:25),
AL035460A S11:	GAGCTTGGGATTGCTGACGCT	(SEQ ID NO:26), and
AL035460A S12:	GCGTCAGCAATCCCAAGCTC	(SEQ ID NO:27).

The sequence of the insert was verified as an open reading frame coding for the predicted AL035460A (ACPL1a) mature protein from residues 21 to 734. The clone was named pCR2.1-AL035460.

Example 2. Construction of the mammalian expression vector pCEP4/Sec

A vector, named pCEP4/Sec, for examining expression of ACPLX sequences in mammalian cells was constructed.

The pCEP4/Sec vector was constructed from pcDNA3.1-V5His (Invitrogen, Carlsbad, CA). The following oligonucleotide primers were designed to amplify a fragment from the expression vector pcDNA3.1-V5His expression vector.

pSec-V5-His Forward CTCGTCCTCGAGGGTAAGCCTATCCCTAAC (SEQ ID NO:28) and

pSec-V5-His Reverse CTCGTCGGGCCCCTGATCAGCGGGTTTAAAC (SEQ ID NO:29)

. The PCR product was digested with XhoI and ApaI and ligated into the XhoI/ApaI digested pSecTag2 B vector harboring an Ig kappa leader sequence (Invitrogen, Carlsbad CA). The correct structure of the resulting vector, pSecV5His, including an in-frame Ig-kappa leader and V5-His6 was verified by DNA sequence analysis. The vector pSecV5His was digested with PmeI and NheI to provide a fragment retaining the above elements in the correct frame. The PmeI-NheI fragment was ligated into the BamHI/Klenow and NheI treated vector pCEP4 (Invitrogen, Carlsbad, CA). The resulting vector was named pCEP4/Sec and includes an in-frame Ig kappa leader, a site for insertion of a clone of interest, V5 and His6 under control of the PCMV and/or the PT7 promoter. PCEP4/Sec is an expression vector that allows heterologous protein expression and secretion by fusing any protein to the Ig Kappa chain signal peptide. Detection and purification of the expressed protein are aided by the presence of the V5 epitope tag and 6xHis tag at the C-terminus (Invitrogen, Carlsbad, CA).

Example 3. Expression of ACPL1a in human embryonic kidney 293 cells.

The 2.1 kb BglII-XhoI fragment containing the human ACPL1a sequence was isolated from pCR2.1-AL035460A (see Example 2) and subcloned into BglII-XhoI digested pCEP4/Sec to generate the expression vector pCEP4/Sec-AL035460. The pCEP4/Sec-AL035460A vector was transfected into 293 cells using the LipofectaminePlus reagent following the manufacturer's instructions (Gibco/BRL, Rockville, MD). The cell pellet and supernatant were harvested 72 hours after transfection and examined for ACPL1a expression by Western blotting (reducing conditions) with an anti-V5 antibody. The molecular weight predicted for the mature fragment of hAL035460, including four amino acid residues encoded by the primers, is 80132 Da. FIG. 6 shows that a monomeric form of hAL035460A is expressed as a predominant band of 125 kDa protein secreted by 293 cells. The mature fragment of AL035460A (ACPL1a) is predicted to have six potential sites for N-glycosylation. The discrepancy between the predicted molecular weight and the observed value is ascribed to glycosylation of the protein, which retards its migration in the gel. In addition, several higher molecular weight bands indicate oligomerization of the secreted ACPL1 protein.

Example 4. Expression analysis using clone ACPL1a.

The expression of sequences homologous to clone ACPL1a was assessed in 41 normal and 55 tumor samples by real time quantitative PCR (TAQMAN®) performed on a Perkin-

Elmer Biosystems ABI PRISM® 7700 Sequence Detection System. In Table BB, the following abbreviations are used:

ca. = carcinoma,

* = established from metastasis,

met = metastasis,

s cell var= small cell variant,

non-s = non-sm =non-small,

squam = squamous,

pl. eff = pl effusion = pleural effusion,

glio = glioma,

astro = astrocytoma, and

neuro = neuroblastoma.

Table IV. Tissue Samples used in Expression Analysis.

No.	Tissue Sample	No.	Tissue Sample
1	Endothelial cells	49	Renal ca. 786-0
2	Endothelial cells (treated)	50	Renal ca. A498
3	Pancreas	51	Renal ca. RXF 393
4	Pancreatic ca. CAPAN 2	52	Renal ca. ACHN
5	Adipose	53	Renal ca. UO-31
6	Adrenal gland	54	Renal ca. TK-10
7	Thyroid	55	Liver
8	Salivary gland	56	Liver (fetal)
9	Pituitary gland	57	Liver ca. (hepatoblast) HepG2
10	Brain (fetal)	58	Lung
11	Brain (whole)	59	Lung (fetal)
12	Brain (amygdala)	60	Lung ca. (small cell) LX-1
13	Brain (cerebellum)	61	Lung ca. (small cell) NCI-H69
14	Brain (hippocampus)	62	Lung ca. (s.cell var.) SHP-77
15	Brain (hypothalamus)	63	Lung ca. (large cell)NCI-H460
16	Brain (substantia nigra)	64	Lung ca. (non-sm. cell) A549
17	Brain (thalamus)	65	Lung ca. (non-s.cell) NCI-H23
18	Spinal cord	66	Lung ca (non-s.cell) HOP-62
19	CNS ca. (glio/astro) U87-MG	67	Lung ca. (non-s.cl) NCI-H522
20	CNS ca. (glio/astro) U-118-MG	68	Lung ca. (squam.) SW 900
21	CNS ca. (astro) SW1783	69	Lung ca. (squam.) NCI-H596
22	CNS ca.* (neuro; met) SK-N-AS	70	Mammary gland
23	CNS ca. (astro) SF-539	71	Breast ca.* (pl. effusion) MCF-7
24	CNS ca. (astro) SNB-75	72	Breast ca.* (pl.ef) MDA-MB-231
25	CNS ca. (glio) SNB-19	73	Breast ca.* (pl. effusion) T47D
26	CNS ca. (glio) U251	74	Breast ca. BT-549
27	CNS ca. (glio) SF-295	75	Breast ca. MDA-N
28	Heart	76	Ovary
29	Skeletal muscle	77	Ovarian ca. OVCAR-3

30	Bone marrow	78	Ovarian ca. OVCAR-4
31	Thymus	79	Ovarian ca. OVCAR-5
32	Spleen	80	Ovarian ca. OVCAR-8
33	Lymph node	81	Ovarian ca. IGROV-1
34	Colon (ascending)	82	Ovarian ca.* (ascites) SK-OV-3
35	Stomach	83	Myometrium
36	Small intestine	84	Uterus
37	Colon ca. SW480	85	Placenta
38	Colon ca.* (SW480 met)SW620	86	Prostate
39	Colon ca. HT29	87	Prostate ca.* (bone met)PC-3
40	Colon ca. HCT-116	88	Testis
41	Colon ca. CaCo-2	89	Melanoma Hs688(A).T
42	Colon ca. HCT-15	90	Melanoma* (met) Hs688(B).T
43	Colon ca. HCC-2998	91	Melanoma UACC-62
44	Gastric ca.* (liver met) NCI-N87	92	Melanoma M14
45	Bladder	93	Melanoma LOX IMVI
46	Trachea	94	Melanoma* (met) SK-MEL-5
47	Kidney	95	Melanoma SK-MEL-28
48	Kidney (fetal)	96	Melanoma UACC-257

96 RNA samples were analyzed. Expression was compared to a reference RNA. In particular, samples were normalized to β-actin and GAPDH. RNA (~50 ng total or ~1 ng polyA+) was converted to cDNA using the TAQMAN® Reverse Transcription Reagents Kit (PE Biosystems, Foster City, CA; cat # N808-0234) and random hexamers according to the manufacturer's protocol. Reactions were performed in 20 ul and incubated for 30 min. at 48^{0}C. cDNA (5 ul) was then transferred to a separate plate for the TAQMAN® reaction using β-actin and GAPDH TAQMAN® Assay Reagents (PE Biosystems; cat. #'s 4310881E and 4310884E, respectively) and TAQMAN® universal PCR Master Mix (PE Biosystems; cat # 4304447) according to the manufacturer's protocol. Reactions were performed in 25 ul using the following parameters: 2 min. at 50^{0}C; 10 min. at 95^{0}C; 15 sec. at 95^{0}C/1 min. at 60^{0}C (40 cycles). Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between two samples being represented as 2 to the power of delta CT. The average CT values obtained for ß-actin and GAPDH were used to normalize RNA samples. The RNA sample generating the highest CT value required no further diluting, while all other samples were diluted relative to this sample according to their β-actin /GAPDH average CT values.

Normalized RNA (5 ul) was converted to cDNA and analyzed via TAQMAN® using One Step RT-PCR Master Mix Reagents (PE Biosystems; cat. # 4309169) and gene-specific primers according to the manufacturer's instructions. Probes and primers were designed for the assay according to Perkin Elmer Biosystem's *Primer Express* Software package (version I

for Apple Computer's Macintosh Power PC) using the sequence of cloneAL035460A as input. Two sets of primers (forward and reverse) and probe were developed, shown below.

Set Ag 86 targets the sequence 267-342.

Ag86 (F): 5'-GTCTGGAGTCCCTGCGAGTTT-3' (SEQ ID NO:30)

Ag86 (R): 5'-CGGTGTGGTCCAAGACCAA-3' (SEQ ID NO:31)

Ag86 (P): TET-5'-CTTGAGGCATCCAGCAGCCAGTCC-3'-TAMRA (SEQ ID NO:32)

Set Ag 86b targets the sequence 271-346.

AG 86(b) (F): 5'-GAGTCCCTGCGAGTTTCAGATAG-3' (SEQ ID NO:33)

AG 86(b) (R): 5'-GTCCTCGGTGTGGTCCAAGA-3' (SEQ ID NO:34)

AG 86(b) (P): TET-5'-TGAGGCATCCAGCAGCCAGTCCTTT-3'-TAMRA (SEQ ID NO:35)

Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60° C, primer optimal Tm = 59° C, maximum primer difference = 2° C, probe does not have 5' G, probe T_m must be 10° C greater than primer T_m, amplicon size 75 bp to 100 bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900 nM each, and probe, 200nM.

PCR conditions: Normalized RNA from each tissue and each cell line was spotted in each well of a 96 well PCR plate (Perkin Elmer Biosystems). PCR cocktails including two probes (ALCLPLX-specific and another gene-specific probe multiplexed with the ALCLPX probe) were set up using 1X TaqMan™ PCR Master Mix for the PE Biosystems 7700, with 5 mM MgCl2, dNTPs (dA, G, C, U at 1:1:1:2 ratios), 0.25 U/ml AmpliTaq Gold™ (PE Biosystems), and 0.4 U/μl RNase inhibitor, and 0.25 U/μl reverse transcriptase. Reverse transcription was performed at 48° C for 30 minutes followed by amplification/PCR cycles as follows: 95° C 10 min, then 40 cycles of 95° C for 15 seconds, 60° C for 1 minute.

The results for probe set Ag86 are presented in FIGS. 6A-C. Highest expression was found in the normal tissues fetal kidney, ovary, mammary gland, placenta and myometrium, with moderate levels of expression in other normal tissues. Use of probe set AG86b detected high expression levels in the same tissues as well as adipose, and moderate levels in other normal tissues (FIGS. 7A-C).

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For cloneAL035460A, the following primers and probes, which detect positions 588-663 in the clone, were used:

Ag 2(F): 5'-GTGCTGCTGCTCTACAATAACCA-3' (SEQ ID NO:36)
Ag 2(R): 5'-GTTTCTGCAGCTGGGCCAT-3' (SEQ ID NO:37)
Ag 2(P):-FAM-5'-TGGACCGGTGCGCCTTCGAT-3'-TAMRA (SEQ ID NO:38)

The results are shown in FIGS. 7A-7C. High expression of clone AL035460A was found in most normal brain tissues tested. In addition, low levels of expression are found in many other normal tissues and certain cancer tissues.

Example 5. Suppression of tumor growth by ACPL1a.

Breast and ovarian tumor cell lines are transfected with the ACPL1a gene under the control of an inducible promoter. Cell lines that may be used include breast carcinoma (pleural effusion) MCF-7, breast carcinoma (pleural effusion) MDA-MB-231, breast carcinoma (pleural effusion) T47D, breast carcinoma BT-549, breast carcinoma MDA-N, ovarian carcinoma OVCAR-3, ovarian carcinoma OVCAR-4, ovarian carcinoma OVCAR-5, ovarian carcinoma OVCAR-8, ovarian carcinoma IGROV-1, and ovarian carcinoma (ascites) SK-OV-3; these cell lines show reduced expression of ACPL1a. Stable transfectants are to be generated using methods based, for example, on incorporating the ACPL1a gene into a mammalian expression vector such as pCDM8 (Seed (1987) *Nature* 329:840) or pMT2PC (Kaufman *et al.* (1987) *EMBO J* 6: 187-195). An inducible promoter may be chosen from among those reviewed in Saez E, et al. (Inducible gene expression in mammalian cells and transgenic mice. Curr Opin Biotechnol 1997 Oct;8(5):608-16). For other suitable expression systems for eukaryotic cells are described, *e.g.*, in Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989. Stable genetic transformation of mammalian cells is also described by Sawada M, and Kamataki T. (Genetically engineered cells stably expressing cytochrome P450 and their application to mutagen assays. Mutat Res. 1998 Aug;411(1):19-43) and DeCruz EE, et al. (The basis for somatic gene therapy of cancer. J Exp Ther Oncol. 1996 Mar;1(2):73-83). Transfection may be effected, for example, by liposome-mediated transfection (Schenborn ET, and Oler J.

Methods Mol Biol. 2000;130:155-64), DEAE-dextran transfection (Schenborn ET, and Goiffon V. Methods Mol Biol. 2000;130:147-53) or calcium phosphate transfection (Schenborn ET, and Goiffon V. (Methods Mol Biol. 2000;130:135-45).

After transfecting the cells, the effect of the ACPL1a gene product on cell growth is be assessed following induction. Both *in vitro* and *in vivo* growth is to be monitored and compared to growth of tumor cells transfected with empty vector. It is expected that the transfected tumor cells will exhibit a decrease in growth rate both *in vitro* and *in vivo* following expression of ACPL1a.

Example 6. Identification of nucleic acid sequences encoding carboxypeptidases.

Genomic clone AL035460.15 on chromosome 20 was identified by TBLASTN using CuraGen Corporation's sequence file for members of splice variant of carboxypeptidase and/or the carboxypeptidase family, run against the genomic daily files made available by GenBank or obtained from Human Genome Project Sequencing centers. These sequences were analyzed for putative coding regions as well as for similarity to known DNA and protein sequences using programs such as Grail, Genscan, BLAST, HMMER, FASTA, Hybrid. Putative coding regions were spliced from the genomic clone and then concatenated using a known homolog for reference.

Some additional genomic regions may have also been identified from proprietary assemblies that map to those regions. The sequences so identified were manually assembled and then extended using one or more additional sequences taken from CuraGen Corporation's human SeqCalling database. Such sequences were included in the derivation of Acc. Nos. CG54007-04 (ACPL2) (SEQ ID NO:5) and CG54007-05 (ACPL3) (SEQ ID NO:7) because the extent of identity in the overlap region with SeqCalling assemblies 173572850 167968540 was high. The extent of identity may be, for example, about 90% or higher, preferably about 95% or higher, and even more preferably close to or equal to 100%.

The DNA sequences and protein sequences for two novel splice variants of a carboxypeptidase-like gene that resulted are reported here as CuraGen Acc. Nos. CG54007-04 (ACPL2) (SEQ ID NO:5) and CG54007-05 (ACPL3) (SEQ ID NO:7).

Example 7. Verification of the sequence of the polypeptide SEQ ID NO:2.

A nucleic acid sequence designated Acc. No. CG54007-06 (ACPL1c) was derived by laboratory cloning using exon linking.

The cDNA coding for ACPL1c was cloned by the polymerase chain reaction (PCR) using the primers:

5'-GACGTGGGATGCACACAGCTC-3' (SEQ ID NO:39) and

5'-GCTGCACTGCTCTGGGGTCA-3' (SEQ ID NO:40).

Primers were designed based on *in silico* predictions of the full length or some portion (one or more exons) of the cDNA/protein sequence of the invention. These primers were used to amplify a cDNA from a pool containing expressed human sequences derived from the following tissues: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea and uterus.

Multiple clones were sequenced and these fragments were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp.

The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clone 130282::156264533.698712.E16.

Example 8. Tryptic digestion and sequencing of the mature form of the carboxypeptidase protein.

The protein produced using clone pCEP4/Sec-AL035460 (Example 3) was subjected to partial digestion with trypsin. 14 μg/mL of trypsin was added to 50 μL of a solution 1 μg/mL of the purified protein and incubated for 12 h at pH 7.5 and 25 °C. The digestion mixture was electrophoresed on SDS-PAGE (4-20% in tris/glycine) and transferred to a PVDF membrane. A Coomassie stained image of the membrane is shown in FIG. 17A. The arrow shows a band

with an apparent molecular weight of approximately 40 kDa. This band was subjected to Edman degradation to determine the N-terminal sequence of the peptide. The result is shown in FIG. 17B. The upper row in Panel B shows a portion of the sequence of SEQ ID NO:2 beginning at position 80 (corresponding to position 60 of the protein produced by clone pCEP4/Sec-AL035460). The lower row shows the actual sequence determined in the Edman procedure. The match is almost perfect (it is felt that the differences arise from Edman sequencing artifacts rather than from mutations in the construct). It is concluded that the 40kDa fragment represents a portion of the sequence of the carboxypeptidase of the invention beginning at position 80 of SEQ ID NO:2. This result provides experimental verification that clone pCEP4/Sec-AL035460 encodes the protein expected for the carboxypeptidase of the invention.

Example 9. Incorporation of BrdU into DNA.

HEK293 cells were transfected with pCEP4sec or pCEP4/Sec-AL035460A vectors (see Example 3) using Lipofectamine 2000 according to the manufacturer's specifications (Gibco/BRL, Rockville, MD). Cells were incubated for 2 d with Dulbecco's modified Eagle's medium (DMEM). Conditioned medium was prepared by collection of cell supernatants. The supernatant was concentrated ten-fold and dialyzed into PBS. The supernatant was enriched by Talon metal affinity chromatography (Clontech, Palo Alto, CA). Briefly, 7 mL of conditioned medium was incubated with 1 mL of a suspension of Talon metal affinity resin. Spin columns were washed twice with 1 mL of PBS. The columns were then eluted twice with 0.65 ml of PBS/0.5M imidazole pH 8.0 and the eluates were pooled. Imidazole was removed by buffer exchange dialysis into PBS using a Microcon centrifugal filter device. Enriched proteins were stored at 4°C.

NIH 3T3 cells (ATCC, No. CRL-1658, Manassas, VA) were cultured in DMEM supplemented with 10% fetal bovine serum or 10% calf serum. Cells were grown to confluence at 37°C in 10% CO_2/air. Cells were then starved in DMEM for 24-72 h. Conditioned medium from the pCEP4sec or pCEP4/Sec-AL035460A transfected HEK293 cells was added (10 μL/100 μL of culture) and the cells were incubated for 18 h. Bromodeoxyuridine (BrdU; 10 μM final concentration) was then added and incubated with the cells for 5 h. BrdU incorporation was assayed using an immunoassay according to the manufacturer's specifications (Boehringer Mannheim, Indianapolis, IN). The results are

shown in FIG. 19 It is seen that the AL035460A (ACPL1a) carboxypeptidase induces the incorporation of BrdU into NIH 3T3 cells.

Example 10. Cell Proliferation Assay

Proliferation activity was measured by treatment of cultured NIH 3T3 cells with the carboxypeptidase of the invention and determining changes in cell number. The cells were grown to 80-90% confluence in DMEM with 10% calf serum. Cells were then treated with 1 μg/mL of purified conditioned medium from the pCEP4sec or pCEP4/Sec-AL035460A transfected HEK293 cells (Example 9) at a concentration of 1 ug/ml and incubated for two days. Cells were photographed with a Zeiss Axiovert 100. Cell numbers were determined by trypsinization followed by counting using a Coulter Z1 Particle Counter. The results of the proliferation assay are shown in FIG. 20. It is seen that the ACPL1a carboxypeptidase induces the proliferation of NIH 3T3 cells.

OTHER EMBODIMENTS

While the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.